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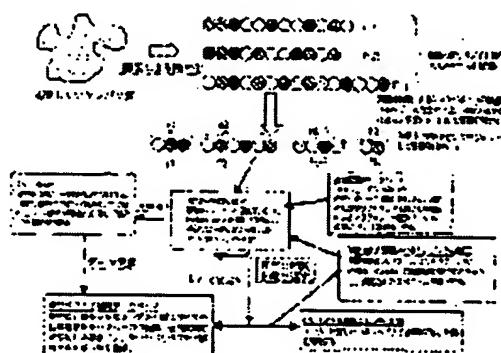
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(54) METHOD AND SYSTEM FOR ANALYZING PROTEOME

(57)Abstract:

PROBLEM TO BE SOLVED: To provide a method and a system that can reduce the number of experiments in identification with a small amount of a sample and an experiment for trial-and-error, adds a mass spectrum that may appear, a peak or the like buried in noise, or the like for achieving a high accuracy in protein identification and high throughput, and can determine sequencing using mass spectrometry even in new protein that is not registered in a protein sequencing database.



SOLUTION: In the mass spectrometry due to a tandem type mass spectrometry apparatus, bond dissociation energy is calculated by using a molecular simulation method, the prediction information of the cleavage pattern of peptide and/or the peak position of the mass spectrum and/or the intensity ratio of a spectrum is added to obtained experiment information for use as the identification of protein.

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